

SEQUENCE LISTING

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Steve Chappell Mitchell
Douglas C. Saffran

<120> NOVEL G PROTEIN-COUPLED RECEPTOR
UP-REGULATED IN PROSTATE CANCER AND USES THEREOF

<130> 129.24USU1

<150> 60/157,902

<151> 1999-10-05

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<170> FastSEQ for Windows Version 4.0

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1 5 10	

ttc atc cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg	219
Phe Ile Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu	
15 20 25	

gcc ttc cca ttg tgc tcc ctc tac ctt att gct gtg cta ggt aac ttg	267
Ala Phe Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu	
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aca atc atc tac att gtg cgg act gag cac agc ctg cat gag ccc atg	315
Thr Ile Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met	
50 55 60	

tat ata ttt ctt tgc atg ctt tca ggc att gac atc ctc atc tcc acc	363
Tyr Ile Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr	
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tca tcc atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc	411
Ser Ser Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr	
80 85 90	

atc cag ttt gat gct tgt ctg cta cag att ttt gcc atc cac tcc tta	459
Ile Gln Phe Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu	
95 100 105	

tct ggc atg gaa tcc aca gtg ctg ctg gcc atg gct ttt gac cgc tat	507
Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr	
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Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro	
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Arg Val Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu	
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Asn Ile Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu	
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Leu Ile Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys	
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gca ttt ggc act tgc gtc tct cat gtg tgt gct gtg ttc ata ttc tat	891
Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr	
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35 40 45
Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
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Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met
65 70 75 80
Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe
85 90 95
Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu Ser Gly Met
100 105 110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115 120 125
Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr
130 135 140
Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro
145 150 155 160
Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu
165 170 175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp
180 185 190
Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala
195 200 205
Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu
210 215 220
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly
225 230 235 240
Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe

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245 250 255
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 260 265 270
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 35 40 45
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50 55 60
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65 70 75 80
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
 85 90 95
 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
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 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
 130 135 140
 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
 210 215 220
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
 260 265 270
 Val Leu Met Gly Asp Val Tyr Leu Leu Pro Pro Val Ile Asn Pro
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35 40 45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
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65 70 75 80
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Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
100 105 110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
115 120 125
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130 135 140
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Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
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Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
195 200 205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
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tataattatt	aatatcctga	ctaggttggtg	gttgagggtg	tattactttt	cattttacca	240
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acatctagag	aacatttgcc	aaaggcctaa	gcacagcaaa	ggaaaataaa	cacagaatat	360
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tct tat atc ttt atc ctt cag gca gtt cta caa ctc tcc tct cag gag 96
Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln Leu Ser Ser Gln Glu
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gcc cgc tac aaa gca ttt ggg aca tgt gtc tct cac ata ggt gcc atc 144
Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser His Ile Gly Ala Ile
35 40 45

tta gcc ttc tac aca cct tca gtc atc tct tca gtc atg cac cgt gtg 192
Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser Val Met His Arg Val
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gcc cgc tgt gct gtg cca cac gtc cac att ctc ctc gcc aat ttc tat 240
Ala Arg Cys Ala Val Pro His Val His Ile Leu Leu Ala Asn Phe Tyr
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Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Lys Thr
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aag cag atc cgt gac agt ctt ggg agt att cct gag aaa gga tgt gtg 336
Lys Gln Ile Arg Asp Ser Leu Gly Ser Ile Pro Glu Lys Gly Cys Val
100 105 110

aat aga gag tga gga ata agt gga aaa aga gtg ggg ccc agt gaa tgc 384
Asn Arg Glu * Gly Ile Ser Gly Lys Arg Val Gly Pro Ser Glu Cys
115 120 125

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Cys Ser Gly Pro Gly Leu Cys * Glu * Met Gly Pro Arg Leu His
130 135 140

gtt tag ttc ttt tct tgt att atg aaa aga ata aat gat gtc ctg aag 480
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Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser His Ile Gly Ala Ile
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Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser Val Met His Arg Val
50 55 60

Ala Arg Cys Ala Val Pro His Val His Ile Leu Leu Ala Asn Phe Tyr

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Lys	Gln	Ile	Arg	Asp	Ser	Leu	Gly	Ser	Ile	Pro	Glu	Lys	Gly	Cys	Val
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Ser	Gly	Pro	Gly	Leu	Cys	Glu	Met	Gly	Pro	Arg	Leu	His	Val	Phe	Phe
	130					135				140					
Ser	Cys	Ile	Met	Lys	Arg	Ile	Asn	Asp	Val	Leu	Lys	Leu	Arg	Lys	Lys
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